

Thu Jan 24 07:40:21 2002

us-09-531-438-4.oli.rng

Page 1

GenCore version 4.5
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ON nucleic - nucleic search, using sw model

Run on: January 24, 2002, 03:28:19 : Search time 222.28 Seconds

(without alignments)
347.126 Million cell updates/sec

Title: US-09-531-438-4

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Gapop 60.0, Capext 60.0

Searched: 930621 seqs, 428662619 residues

Word size: 0

Total number of hits satisfying chosen parameters: 98696

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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22: /SID52/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	15.6	20	AA205048	PCR primer used to
2	14	15.6	26	AAV07952	Helicobacter pylori
3	14	15.6	26	AAV07952	Helicobacter pylori
4	14	15.6	27	AAV07937	Helicobacter pylori
5	14	15.6	47	AA268842	Human map-related
6	14	15.6	17	AA093084	Renilla reniformis
7	14	15.6	20	AAK93307	PCR primer used to
8	14	15.6	23	AAH27610	Human lipoprotein
9	14	15.6	24	AAH55939	Human SCN1A PCR-SS
10	14	15.6	26	AA068537	B. thuringiensis 33
11	14	15.6	26	AA067312	Alzheimer's disease

12	13	14.4	26	21	AA067342	Alzheimer's disease
13	13	14.4	31	19	AAV07957	Helicobacter pylori
14	13	14.4	34	16	AAH15377	A2F ASF cosmid c10
15	13	14.4	35	22	AAH61207	Coxsackie virus B
16	13	14.4	36	22	AAH90560	Dissociation trans
17	13	14.4	38	17	AAH34130	III. promoter-RTV-
18	13	14.4	39	13	AA035630	HIV-2 env 3', fragm
19	13	14.4	39	14	AA035353	PCR primer HIV2B2.
20	13	14.4	39	21	AAH99138	Plasmid pDMPTC PC
21	13	14.4	40	21	AAH61322	Insecticidal prote
22	13	14.4	40	21	AAH61323	Primer 3A used to
23	13	14.4	41	19	AAH51009	Maize polymorphic
24	13	14.4	41	19	AAH51011	Maize polymorphic
25	13	14.4	50	16	AAH25074	Human gene signatu
26	13	14.4	50	20	AAH52184	Synthetic plasmid
27	13	14.4	50	20	AAH52048	Synthetic plasmid
28	13	14.4	50	20	AAH70046	Human fli1 VEGF re
29	13	14.4	17	18	AAH70047	Human fli1 VEGF re
30	13	14.4	17	18	AAH70047	Human fli1 VEGF re
31	13	14.4	17	18	AAH21453	Integrin alpha 6 s
32	13	14.4	17	20	AAH21454	Integrin alpha 6 s
33	13	14.4	17	20	AAH21455	Integrin alpha 6 s
34	13	14.4	17	21	AAH03088	Hammerhead ribozym
35	13	14.4	17	21	AAH03089	Hammerhead ribozym
36	13	14.4	17	21	AAH03090	Hammerhead ribozym
37	13	14.4	17	21	AAH03091	Hammerhead ribozym
38	13	14.4	18	21	AAH08821	Human survivin DNA
39	13	14.4	19	15	AAH062806	Env gene 5' primer
40	13	14.4	19	21	AAH69625	Human blattellie ma
41	13	14.4	19	21	AAH75126	HIV RNA translati
42	13	14.4	20	11	AAH05907	Staphylococcus aur
43	13	14.4	20	19	AAH72697	Corn kernel oil co
44	13	14.4	20	19	AAH72697	PCR primer used to
45	13	14.4	20	20	AAH92327	

ALIGNMENTS

RESULT 1

ID: AA205048 standard: DNA: 20 BP.

AA205048:

07-OCT-1999 (first entry)

PCR primer used to amplify an ORF of Chlamydia trachomatis.

Vaccine: eye disease; conventional trachoma; nonendemic trachoma;

paratrachoma; inclusion conjunctivitis; genital disease; perithenitis;

KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;

bartholinitis; pneumonia; venereal lymphogranulomatosis; ss.

Synthetic.

Chlamydia trachomatis.

W09928475-A2.

10-JUN-1999.

27-NOV-1998; 98MO-IB01939.

04-NOV-1998; 98US-0107077.

28-NOV-1997; 97ER-0015041.

17-DEC-1997; 97ER-0016034.

(GEST) GENSET.

Griffiths R;

WPI: 1999-371125/31.

PT Genome sequence of Chlamydia trachomatis
XX
PS Disclosure: Page 1738; 1755pp: English.
XX
XX PCR primers AA201426-206209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs
CC encode polypeptides (see AAY35754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences
CC can also be used to control growth of the microorganism. Chlamydia
CC trachomatis is responsible for a large number of diseases, e.g. eye
CC diseases such as conventional trachoma, nongonococcal urethritis,
CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
CC peritonitis, Bartholinitis; pneumonia in breast feeding infants;
CC and venereal lymphogranulomatosis. The polypeptides of the
CC invention may be of use in treating these diseases.
XX
XX
XX Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 other:

Query Match 15.6%; Score 14; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 54 ttattgttgagca 67
|||||
DB 4 ttattgttgagca 17

RESULT 2

AAV07952/C
ID AAV07952 standard; DNA; 26 BP.

AAV07952:

02-FEB-1999 (first entry)

Helicobacter pylori polypeptide GHPO 1414 5' DNA primer.

GHPO 1414; Infection; gastritis; ulcer; vaccine; diagnosis;
therapy; PCR; primer; ss.

Synthetic.
Helicobacter pylori.

MO9843479-A1.

08-OCT-1998.

31-MAR-1998; 98MO-US06421.

01-APR-1997; 97US-0834666.

01-APR-1997; 97US-0831310.

(HUMA-) HUMAN GENOME SCI INC.
(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS ET VACCINS.

Al-Garawi A, Kleanthous H, Lissolo L, Miller C, Tomb J;
WPI: 1998-568251/48.

New isolated Helicobacter polynucleotides - used to develop products
for the diagnosis, prevention and treatment of Helicobacter
infections and gastroduodenal diseases

Claim 5; Page 145; 184pp: English.

This 5' primer is used with a 3' primer (see AAV07954) in the PCR
amplification of Helicobacter, e.g. Helicobacter pylori, genomic
DNA in order to obtain DNA (see AAV07921) encoding the unprocessed
form of a 76 kDa polypeptide (see AAV73032) designated GHPO 1414.
The isolated polynucleotide, and encoded polypeptide, can be used
to develop vaccines for the treatment and prevention of Helicobacter

CC Infections.
XX
XX Sequence 26 BP; 14 A; 5 C; 4 G; 3 T; 0 other:

Query Match 15.6%; Score 14; DB 19; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 40 ttctcatgtttct 53
|||||
DB 18 TTTTCATGTTTCT 5

RESULT 3

AAV07922/C
ID AAV07922 standard; DNA; 26 BP.

AAV07922:

02-FEB-1999 (first entry)

Helicobacter pylori polypeptide GHPO 386 5' DNA primer.

GHPO 386; Infection; gastritis; ulcer; vaccine; diagnosis; therapy;
PCR; primer; ss.

Synthetic.
Helicobacter pylori.

MO9843479-A1.

08-OCT-1998.

31-MAR-1998; 98MO-US06421.

01-APR-1997; 97US-0834666.

01-APR-1997; 97US-0831310.

(HUMA-) HUMAN GENOME SCI INC.
(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS ET VACCINS.

Al-Garawi A, Kleanthous H, Lissolo L, Miller C, Tomb J;
WPI: 1998-568251/48.

New isolated Helicobacter polynucleotides - used to develop products
for the diagnosis, prevention and treatment of Helicobacter
infections and gastroduodenal diseases

Claim 5; Page 137; 184pp: English.

This 5' primer is used with a 3' primer (see AAV07924) in the PCR
amplification of Helicobacter, e.g. Helicobacter pylori, genomic
DNA in order to obtain DNA (see AAV72001
CC) encoding the unprocessed
CC form of a 76 kDa polypeptide (see AAV73032) designated GHPO 386. The
CC isolated polynucleotide, and encoded polypeptide, can be used to
CC develop vaccines for the treatment and prevention of Helicobacter
CC infections.

Sequence 26 BP; 15 A; 5 C; 4 G; 2 T; 0 other:

Query Match 15.6%; Score 14; DB 19; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 40 ttctcatgtttct 53
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DB 20 TTTTCATGTTTCT 7

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OM nucleic - nucleic search, using SW model

Run on: January 24, 2002, 02:22:33 : Search time 93.51 Seconds
(without alignments)
791.983 Million cell updates/sec

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Gapop 60.0, Gapext 60.0

Searched: 351203 seqs, 113238999 residues

Word size : 5 0

Total number of hits satisfying chosen parameters: 495388

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	16	4.9	29	3 US-08-816-977-12	Sequence 12, Appl
2	16	4.9	36	1 US-08-639-600-16	Sequence 16, Appl
3	15	4.6	27	1 US-08-120-827-66	Sequence 66, Appl
4	15	4.6	27	1 US-08-478-675-66	Sequence 66, Appl
5	15	4.6	30	5 PCT-US92-10792-3	Sequence 3, Appl
6	15	4.6	32	1 US-08-256-261-29	Sequence 29, Appl
7	15	4.6	32	3 US-08-852-299-29	Sequence 29, Appl
8	14	4.3	18	2 US-09-205-204-20	Sequence 20, Appl
9	14	4.3	29	3 US-08-816-977-12	Sequence 12, Appl
10	14	4.3	30	2 US-08-639-001A-31	Sequence 31, Appl
11	14	4.3	30	4 US-08-642-274D-110	Sequence 110, Appl
12	14	4.3	36	1 US-08-639-600-16	Sequence 16, Appl
13	14	4.3	37	2 US-08-403-853-8	Sequence 8, Appl
14	14	4.0	18	3 US-08-847-844A-113	Sequence 113, Appl
15	14	4.0	18	4 US-08-686-968C-13	Sequence 13, Appl
16	14	4.0	20	3 US-09-288-461-79	Sequence 79, Appl
17	14	4.0	21	3 US-08-691-045-61	Sequence 61, Appl
18	14	4.0	24	3 US-08-672-115-1	Sequence 1, Appl
19	14	4.0	28	1 US-08-130-827-64	Sequence 64, Appl
20	14	4.0	28	1 US-08-478-675-64	Sequence 64, Appl
21	14	4.0	30	2 US-08-639-001A-79	Sequence 79, Appl
22	14	4.0	30	4 US-08-642-274D-158	Sequence 158, Appl
23	13	4.0	31	1 US-08-310-638D-5	Sequence 5, Appl
24	13	4.0	31	2 US-08-906-746A-5	Sequence 5, Appl
25	13	4.0	36	1 US-08-247-809A-14	Sequence 14, Appl
26	13	4.0	36	2 US-08-711-728-14	Sequence 14, Appl
27	13	4.0	37	2 US-08-097-554A-45	Sequence 45, Appl

28	13	4.0	37	2 US-08-484-575A-10	Sequence 10, Appl
29	13	4.0	37	3 US-08-477-459-10	Sequence 10, Appl
30	13	4.0	37	3 US-08-480-640A-45	Sequence 45, Appl
31	13	4.0	37	3 US-08-479-869-10	Sequence 10, Appl
32	13	4.0	37	3 US-08-295-802-45	Sequence 45, Appl
33	13	4.0	37	3 US-08-466-414-10	Sequence 10, Appl
34	13	4.0	37	4 US-08-488-273A-45	Sequence 45, Appl
35	13	4.0	37	5 PCT-US94-01826A-10	Sequence 10, Appl
36	13	4.0	37	5 PCT-US94-02252A-10	Sequence 10, Appl
37	13	4.0	38	5 PCT-US96-00547-40	Sequence 40, Appl
38	13	4.0	39	1 US-08-105-483-168	Sequence 168, Appl
39	13	4.0	39	1 US-08-709-209-168	Sequence 168, Appl
40	13	4.0	39	1 US-08-303-275-56	Sequence 56, Appl
41	13	4.0	39	1 US-08-458-101-168	Sequence 168, Appl
42	13	4.0	39	2 US-09-028-361A-19	Sequence 19, Appl
43	13	4.0	40	1 US-08-199-5078-39	Sequence 39, Appl
44	13	4.0	40	1 US-08-441-828-39	Sequence 39, Appl
45	13	4.0	41	3 US-08-930-503A-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-816-977-12
Sequence 12, Application US/08816977
Patient No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamlin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-816-977-12

Query Match 4.9% Score 16; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
189 aaataatcatctta 204
|||||

Thu Jan 24 07:40:19 2002

us-09-531-438-3.01.rni

Page 2

DB 9 AAAAAAAAAATTTT 24

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RESULT 2
US-08-629-600-16
Sequence 16, Application US/08629600
Patent No. 5783196
GENERAL INFORMATION:
APPLICANT: NORIEGA, Fernando
APPLICANT: LEVINE, Myron M.
TITLE OF INVENTION: GUA MUTANTS OF SHIGELLA
TITLE OF INVENTION: AND VACCINES CONTAINING THE SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGARUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
CITY: Washington, D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/629,600
FILING DATE: 9-APR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-6765
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7060
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-629-600-16

Query Match 4.9% Score 16; DB 1; Length 36;
Best Local Similarity 100.0% Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 189 aaaaattttttttt 204
DB 14 AAAAAAAAAATTTT 29

RESULT 3
US-08-120-827-66
Sequence 66, Application US/08120827
Patent No. 5525495
GENERAL INFORMATION:
APPLICANT: KEENE, JACK D.
APPLICANT: KING, PETER H.
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF
TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P.C. Jefferson Davis Highway, Fourth Floor
STREET: 1735 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
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STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/120,827
FILING DATE: 15-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5525495man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 714-158-0 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: RNA (genomic)
US-08-120-827-66

Query Match 4.6% Score 15; DB 1; Length 27;
Best Local Similarity 33.3% Pred. No. 7.9e+02;
Matches 5; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

OY 197 tatttttttttaa 211
DB 12 UUUUUUUUUUUAAA 26

RESULT 4
US-08-478-675-66
Sequence 66, Application US/08478675
Patent No. 5773246
GENERAL INFORMATION:
APPLICANT: KEENE, JACK D.
APPLICANT: KING, PETER H.
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS
TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P.C.
STREET: 1735 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,675
FILING DATE: 07-JUN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/120,827
FILING DATE: 15-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5773246man F.
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ON nucleic - nucleic search, using sw model

Run on: January 24, 2002, 02:19:03 ; Search time 1494.92 Seconds

3608.606 Million cell updates/sec

Title: US-09-531-438-3
Perfect score: 327

Sequence: 1 atttggaatcctaaatt.....tttcatttcttattgtc 327

Scoring table:

OLIGO_NUC	60.0
Gapop	60.0
Gapext	60.0

Searched: 1472140 seqs, 8248589755 residues

Word size : 0

Total number of hits satisfying chosen parameters:

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

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16:	em.hum:*	
17:	em.in:*	
18:	em.om:*	
19:	em.or:*	
20:	em.ov:*	
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25:	em.stg:*	
26:	em.un:*	
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31:	em.htg.inu:*	
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35:	em.htg.ro:*	
36:	em.htg.other:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	16	4.9	29	6	AR099868	AR099868 Sequence
2	16	4.9	32	6	E27913	E27913 Method for
3	16	4.9	30	3	CEANOMTEF	X97532 C.elegans D
4	16	4.9	36	6	AR019036	AR019036 Sequence
5	15	4.6	27	6	AR014030	AR014030 Sequence
6	15	4.6	27	6	I21980	I21980 Sequence 66
7	15	4.6	33	6	AR037189	AR037189 Sequence
8	14	4.3	33	6	AR076533	AR076533 Sequence
9	14	4.3	29	6	AR099868	AR099868 Sequence
10	14	4.3	30	6	AR028182	AR028182 Sequence
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14	14	4.3	37	6	AR063204	AR063204 Sequence
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16	14	4.3	45	6	AX0498974	AX0498974 Sequence
17	14	4.3	45	6	AX059885	AX059885 Sequence
18	14	4.3	45	6	AX059886	AX059886 Sequence
19	14	4.3	45	6	AX137975	AX137975 Sequence
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21	14	4.3	50	6	AX159885	AX159885 Sequence
22	14	4.0	18	6	AR146953	AR146953 Sequence
23	13	4.0	20	6	AR121058	AR121058 Sequence
24	13	4.0	20	6	AR076045	AR076045 Sequence
25	13	4.0	23	6	A97479	A97479 Sequence 35
26	13	4.0	24	6	AX093544	AX093544 Sequence
27	13	4.0	24	6	AX164353	AX164353 Sequence
28	13	4.0	24	12	AB069100	AB069100 Synthetic
29	13	4.0	25	6	AX042574	AX042574 Sequence
30	13	4.0	25	6	AX043288	AX043288 Sequence
31	13	4.0	26	6	AX039624	AX039624 Sequence
32	13	4.0	26	6	AX039654	AX039654 Sequence
33	13	4.0	28	6	AR014028	AR014028 Sequence
34	13	4.0	28	6	I21978	I21978 Sequence 64
35	13	4.0	29	6	AX012366	AX012366 Sequence
36	13	4.0	29	6	E59972	E59972 Highly actl
37	13	4.0	30	6	AR028230	AR028230 Sequence
38	13	4.0	30	6	AR138633	AR138633 Sequence
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40	13	4.0	31	6	I95122	I95122 Sequence 5
41	13	4.0	33	5	XE1ARSE59	K01606 Xenopus 1de
42	13	4.0	36	6	AX10122	AX10122 Sequence 14
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44	13	4.0	36	6	AX167671	AX167671 Sequence
45	13	4.0	36	6	I28261	Sequence 14

JOURNAL and Immunoregulation
Patent: US 5773246-A 66 30-JUN-1998;
FEATURES Location/Qualifiers
SOURCE 1..27
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BASE COUNT 7 a 2 c 2 g 16 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 197 tattttatttttaa 211
Db 12 TATTTTATTTTAA 26

RESULT 6
LOCUS 121980 27 bp DNA PAT 07-OCT-1996
DEFINITION Sequence 66 from patent US 5525495.
ACCESSION 121980
VERSION 121980.1 GI:1602334
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 27)
AUTHORS Keene,J.D., Levine,T. and Gao,F.
TITLE Methods and compositions useful in the recognition, binding and expression of ribonucleic acids involved in cell growth, neoplasia and immunoregulation
JOURNAL Patent: US 5525495-A 66 11-JUN-1996;
FEATURES Location/Qualifiers
SOURCE 1..27
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ORIGIN

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
LOCUS AR037189 32 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 29 from patent US 5801037.
ACCESSION AR037189
VERSION AR037189.1 GI:5955045
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 32)
AUTHORS Behke,D., Schlotz,B., Albrecht,S., Guhrs,K. and Hartmann,M.
TITLE Expression of signal-peptide-free staphylokinases
JOURNAL Patent: US 5801037-A 29 01-SEP-1998;
FEATURES Location/Qualifiers
SOURCE 1..32
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.4e+04;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 154 aaaggaataataa 168
Db 30 AAAGGAATATATAA 16

RESULT 8
LOCUS AR076353/c 18 bp DNA PAT 30-AUG-2000
DEFINITION Sequence 20 from patent US 5958772.
ACCESSION AR076353
VERSION AR076353.1 GI:10003099
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.Frank, Ackermann,E.J. and Cosset,L.M.
TITLE Antisense inhibition of cellular inhibitor of apoptosis-1 expression
JOURNAL Patent: US 5958772-A 20 28-SEP-1999;
FEATURES Location/Qualifiers
SOURCE 1..18
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Best Local Similarity 100.0%; Pred. No. 6.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 160 aaataataataa 173
Db 18 AAATAAATAATAA 5

RESULT 9
LOCUS AR099868/c 29 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 12 from patent US 6080400.
ACCESSION AR099868
VERSION AR099868.1 GI:12810316
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 29)
AUTHORS Williams,J.A. and Byrne,L.Marie.
TITLE Compositions for the prevention and treatment of verotoxin-induced disease
JOURNAL Patent: US 6080400-A 12 27-JUN-2000;
FEATURES Location/Qualifiers
SOURCE 1..29
/organism="unknown"
BASE COUNT 11 a 2 c 5 g 11 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 189 aaataatttttt 202
Db 22 AAATAATATATTT 9

RESULT 10
LOCUS AR028182 30 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 31 from patent US 5858661.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 24, 2002, 01:12:37 : Search time 1502.85 Seconds

(without alignments)
3589.565 Million cell updates/sec

Title: US-09-531-438-3

Perfect score: 327
Sequence: 1 attggagatacttaatt.....tttcattttcttatgtgt 327

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

GenBdb: 1: gb_ba: 2: gb_hg: 3: gb_in: 4: gb_om: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_scs: 12: gb_sy: 13: gb_un: 14: gb_vl: 15: em_ba: 16: em_fun: 17: em_hum: 18: em_in: 19: em_om: 20: em_of: 21: em_ov: 22: em_pat: 23: em_ph: 24: em_pl: 25: em_ro: 26: em_scs: 27: em_sy: 28: em_un: 29: em_vl: 30: em_hgo_hum: 31: em_hgo_inv: 32: em_hgo_rnd: 33: em_hgo_hum: 34: em_hgo_inv: 35: em_hgo_rnd: 36: em_hgo_other:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	327	100.0	1392	1 L77965	L77965 Clostridium
3	327	100.0	1392	6 AX004613	AX004613 Sequence
4	199	60.9	54310	1 AP003515	AP003515 Clostridi
5	81.8	25.0	12900	3 AF001429	AF001429 Plasmodu
6	79	24.2	39347	9 AL135906	AL135906 Human DNA
7	77.8	23.6	53932	2 AC023371	AC023371 Homo sapi
8	77.4	23.7	163443	2 AC006280	AC006280 Plasmodu
9	77.4	23.7	205429	2 AC005506	AC005506 Plasmodu
10	76.2	23.3	3392	3 AF300334	AF300334 Dictyoste
11	76.2	23.3	242513	2 AF079314	AF079314 Homo sapi
12	75.8	23.2	318251	2 PF0413P3	PF0413P3 Plasmodu
13	75.6	23.1	140414	2 AF377947	AF377947 Oryza sat
14	75	22.9	178783	9 AC068139	AC068139 Homo sapi
15	74.4	22.8	156060	2 AC004153	AC004153 Plasmodu
16	73.2	22.4	863	11 CDS06EVO	AL335628 17 end of
17	73	22.3	862	8 YSCWCTOC	W57514 Saccharomyc
18	72.8	22.3	34119	8 AF222718	AF222718 Chrysodid
19	72.2	22.1	104932	2 AC005504	AC005504 Plasmodu
20	72.2	22.1	162445	2 AL158151	AL158151 Human DNA
21	72.2	22.1	169546	2 AC004157	AC004157 Plasmodu
22	72.2	22.1	199882	9 AL354720	AL354720 Human DNA
23	72	22.0	158398	2 AC011146	AC011146 Homo sapi
24	71.6	21.9	180903	9 AC073409	AC073409 Homo sapi
25	71.4	21.8	12029	3 AB001400	AB001400 Plasmodu
26	71.4	21.8	175053	2 AC090014	AC090014 Homo sapi
27	71.2	21.8	110000	2 AL591074_2	Continuation (3 of
28	71	21.7	95477	2 AC007076	AC007076 Homo sapi
29	71	21.7	168799	9 AC009531	AC009531 Homo sapi
30	71	21.7	194038	9 AC010103	AC010103 Homo sapi
31	70.8	21.6	159475	2 AC021378	AC021378 Homo sapi
32	70.6	21.6	13433	3 AF315648	AF315648 Ceratilis
33	70.6	21.6	85779	8 SCE011856	AJ011856 Saccharom
34	70.6	21.6	122747	2 AC093220	AC093220 Homo sapi
35	70.6	21.6	159255	2 AF212831	AF212831 Homo sapi
36	70.6	21.6	161230	2 AC011355	AC011355 Homo sapi
37	70.6	21.6	234112	3 PF0414P2	AL035475 Plasmodu
38	70.6	21.6	340000	9 HS21C013	AL163213 Homo sapi
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40	70.4	21.5	160624	9 AC060835	AC060835 Homo sapi
41	70.4	21.5	172758	2 AC022553	AC022553 Homo sapi
42	70.4	21.5	199551	2 AC006281	AC006281 Plasmodu
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45	70.2	21.5	183384	9 AC012492	AC012492 Homo sapi

ALIGNMENTS

RESULT 1
AX004614 LOCUS AX004614 327 bp DNA PAT 24-AUG-2000
DEFINITION Sequence 2 from Patent WO9915569.
ACCESSION AX004614
VERSION AX004614.1 GI:9928055

KEYWORDS
SOURCE
ORGANISM

Clostridium perfringens.
Clostridium perfringens
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.

REFERENCE 1 (bases 1 to 327)

AUTHORS Gilbert M. and Popoff M. R.

TITLE Clostridium toxin, and method for preparing immunogenic

COMPOSITIONS

PATENT: WO 9915569-A 2 01-APR-1999;

GIBERT MARISE (FR); PASTEUR INSTITUT (FR)

LOCATION/Qualifiers

1. 327

/organism="Clostridium perfringens"

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